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     FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
     15:53:30 ON 09 AUG 2001
L1            38 S THREONINE AND ((PHOSPHOGLUCOSE (W) ISOMERASE) OR (GLUCOSE (W)
L2            30 DUP REM L1 (8 DUPLICATES REMOVED)
L3            18 S L2 NOT PY>1999
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SWERS - CONTINUE? Y/(N):y

L3 ANSWER 1 OF 18 MEDLINE
ACCESSION NUMBER: 1998391765 MEDLINE
DOCUMENT NUMBER: 98391765 PubMed ID: 9724326
TITLE: Complete sequence of a 93.4-kb contig from chromosome 3 of Trypanosoma cruzi containing a strand-switch region.
AUTHOR: Andersson B; Aslund L; Tammi M; Tran A N; Hoheisel J D; Pettersson U
CORPORATE SOURCE: Department of Genetics and Pathology, Biomedical Center, S-751 23 Uppsala, Sweden.. bjorn.andersson@medgen.uu.se
SOURCE: GENOME RESEARCH, (1998 Aug) 8 (8) 809-16.
Journal code: CES; 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF052831; GENBANK-AF052832; GENBANK-AF052833
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19981006
Last Updated on STN: 20000303
Entered Medline: 19980923

AB We have initiated large-scale sequencing of the third smallest chromosome of the CL Brener strain of Trypanosoma cruzi and we report here the complete sequence of a contig consisting of three cosmids. This contig covers 93.4 kb and has been found to contain 20-30 novel genes and several repeat elements, including a novel chromosome 3-specific 400-bp repeat sequence. The intergenic sequences were found to be rich in di- and trinucleotide repeats of varying lengths and also contained several known T. cruzi repeat elements. The sequence contains 29 open reading frames (ORFs) longer than 700 bp, the longest being 5157 bp, and a large number of shorter ORFs. Of the long ORFs, seven show homology to known genes in parasites and other organisms, whereas four ORFs were confirmed by sequencing of cDNA clones. Two shorter ORFs were confirmed by a database homology and a cDNA clone, respectively, and one RNA gene was identified. The identified genes include two copies of the gene for alanine-aminotransferase as well as genes for **glucose-6-phosphate isomerase**, protein kinases and phosphatases, and an ATP synthase subunit. An interesting feature of the sequence was that the genes appear to be organized in two long clusters containing multiple genes on the same strand. The two clusters are transcribed in opposite directions and they are separated by an approximately 20-kb long, relatively GC-rich sequence, that contains two large repetitive elements as well as a pseudogene for cruzipain and a gene for U2snRNA. It is likely that this strand switch region contains one or more regulatory and promoter regions. The reported sequence provides the first insight into the genome organization of T. cruzi and shows the potential of this approach for rapid identification of novel genes. [The sequence data described in this paper have been submitted to the GenBank data library under accession nos. AF052831-AF052833.]

L3 ANSWER 2 OF 18 MEDLINE
ACCESSION NUMBER: 94364540 MEDLINE
DOCUMENT NUMBER: 94364540 PubMed ID: 8082823
TITLE: Multilocus enzyme typing of human and animal strains of Clostridium perfringens.
AUTHOR: Pons J L; Combe M L; Leluan G
CORPORATE SOURCE: Laboratoire de Microbiologie-Pharmacie, Faculte de Medecine-Pharmacie, Universite de Rouen, Saint-Etienne du Rouvray, France.
SOURCE: FEMS MICROBIOLOGY LETTERS, (1994 Aug 1) 121 (1) 25-30.
Journal code: FML; 7705721. ISSN: 0378-1097.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199410
ENTRY DATE: Entered STN: 19941021
Last Updated on STN: 19941021
Entered Medline: 19941010

AB Multilocus enzyme electrophoresis was developed to evaluate the genetic diversity of 71 human strains and 17 animal strains of Clostridium perfringens. Crude protein extracts, obtained by sonication of washed bacteria, were analyzed by polyacrylamide-agarose gel electrophoresis to characterize electrophoretic mobility variants of seven enzymes (esterase, glutamate dehydrogenase, glutamic-oxaloacetic transaminase, nucleoside phosphorylase, **phosphoglucose isomerase**, phosphoglucomutase, **threonine** dehydrogenase). Genetic diversity of the enzyme loci ranged from 0.340 to 0.813. Sixty-nine electrophoretic

types were described among the 88 strains tested and the index of discrimination was 0.994. All strains were typable, and epidemiological relationships between isolates could be established. This method showed a fair correlation with esterase electrophoretic typing based on hydrolytic and electrophoretic polymorphism of esterases. This work demonstrates that multilocus enzyme polymorphism is a reliable and discriminant marker of genetic diversity of strains of C. perfringens.

L3 ANSWER 3 OF 18 MEDLINE
ACCESSION NUMBER: 86062308 MEDLINE
DOCUMENT NUMBER: 86062308 PubMed ID: 4067875
TITLE: Biochemical identification and phylogenetic relationships in free-living amoebas of the genus Naegleria.
AUTHOR: Pernin P; Cariou M L; Jacquier A
SOURCE: JOURNAL OF PROTOZOOLOGY, (1985 Nov) 32 (4) 592-603.
Journal code: JT3; 2985197R. ISSN: 0022-3921.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198512
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19980206
Entered Medline: 19851226

AB Using isoelectric focusing, the zymograms of 23 pathogenic and nonpathogenic Naegleria strains were studied for the activity of 16 enzymes. Certain enzymes (lactate dehydrogenase, L-**threonine** dehydrogenase, superoxide dismutase, acid phosphatase, malic enzyme, and leucine aminopeptidase) proved particularly useful from a practical point of view as they allow easy and reliable identification of pathogenic N. fowleri and N. australiensis as well as nonpathogenic N. lovaniensis strains. Genetic interpretation of these zymograms gave estimates of genetic distances that largely confirmed the taxonomic position of the Naegleria species. In addition, the genetic data suggest that there are two main phylogenetic groups in the genus Naegleria.

L3 ANSWER 4 OF 18 MEDLINE
ACCESSION NUMBER: 82142214 MEDLINE
DOCUMENT NUMBER: 82142214 PubMed ID: 7037754
TITLE: Altered expression of biodegradative **threonine** dehydratase in Escherichia coli mutants.
AUTHOR: Merberg D; Datta P
CONTRACT NUMBER: GM 21436 (NIGMS)
T32 GM 07315 (NIGMS)
SOURCE: JOURNAL OF BACTERIOLOGY, (1982 Apr) 150 (1) 52-9.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198205
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 19980206
Entered Medline: 19820527

AB A number of strains of Escherichia coli K-12 failed to synthesize significant amounts of biodegradative **threonine** dehydratase (EC 4.2.1.16) when grown anaerobically in tryptone-yeast extract medium, a condition which is optimal for the induction of this enzyme. However, the addition of 10 mM potassium nitrate to the culture medium enabled a few of these strains, notably MB201, to induce the enzyme. An examination of the kinetic parameters, modifier sensitivity, and immunological cross-reactivity revealed that the enzyme produced by MB201 in nitrate-supplemented medium appeared indistinguishable from the dehydratase of a wild-type strain. The reduced expression of **threonine** dehydratase in MB201 appeared highly specific; the synthesis of two other inducible enzymes, D-serine deaminase and tryptophanase, and two "anaerobic" proteins, namely, fumarate reductase and cytochrome c551, remained unaffected. The mutation (tdcI) responsible for the altered expression of the dehydratase in MB201 was located at min 91 on the E. coli chromosome and appeared to tightly linked to if not identical with **pgi**, the gene encoding **phosphoglucose isomerase**, as judged by growth experiments on glucose and fructose, direct assay of **phosphoglucose isomerase** activity, spontaneous and simultaneous reversion of MB201 (tdcI) to TdcI+ and **Pgi**+ phenotype, and cosegregation of the two loci during transduction with P1 phage. Because not all strains lacking the dehydratase showed nitrate-dependent enzyme synthesis or had lesions at the **pgi** locus, it appears that mutations at multiple loci on the E. coli chromosome may influence the expression of the enzyme in vivo.

L3 ANSWER 5 OF 18 MEDLINE
ACCESSION NUMBER: 81122956 MEDLINE
DOCUMENT NUMBER: 81122956 PubMed ID: 6450896
TITLE: The electrophoretic mobilities and activities of eleven enzymes of bloodstream and culture forms of Trypanosoma brucei compared.
AUTHOR: Kilgour V
SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1980 Oct) 2 (1) 51-62.
Journal code: NOR; 8006324. ISSN: 0166-6851.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198104
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19990129
Entered Medline: 19810421

AB Eleven soluble enzymes in the supernatant of bloodstream Trypanosoma brucei were compared for electrophoretic mobility and activity with those of T. brucei cultures grown in 3 different media. All bands of each enzyme found in the bloodstream form were also present in the cultured material, but extra bands of malate dehydrogenase (MDH) (EC 1.1.1.37), aspartate aminotransferase (ASAT) (EC 2.6.1.1), and in 2 to 6 cultures of isocitrate dehydrogenase (ICD) (EC 1.1.1.42) were present in culture forms but not in bloodstream forms. An interfering enzyme, peculiar to cultured T. brucei, which reacted with 2-oxoglutarate and possibly a trace amount of ammonium ions, ran with the fast-moving ASAT bands. **Threonine** dehydrogenase activity, high in cultured trypanosomes irrespective of the medium used but low in bloodstream trypanosomes, was markedly lower in Trypanosoma evansi and a much passaged T. brucei 8/18. Glucosephosphate isomerase activity on the other hand was high in bloodstream and low in cultured trypanosomes. Glutamate dehydrogenase activity was too low to record reliably in bloodstream trypanosomes, but could be clearly detected in cultured forms. As the differences point to some changes in gene expression between the two forms, culture material is likely to replace trypanosomes from living animals for electrophoretic characterization only when considerable comparative work has been done.

L3 ANSWER 6 OF 18 MEDLINE
ACCESSION NUMBER: 77245873 MEDLINE
DOCUMENT NUMBER: 77245873 PubMed ID: 19238
TITLE: Lack of hepatic enzymatic adaptation to low and high levels of dietary protein in the adult cat.
AUTHOR: Rogers Q R; Morris J G; Freedland R A
SOURCE: ENZYME, (1977) 22 (5) 348-56.
Journal code: EI6; 1262265. ISSN: 0013-9432.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197710
ENTRY DATE: Entered STN: 19900314
Last Updated on STN: 19980206
Entered Medline: 19771031

AB The activities of three urea cycle enzymes, several nitrogen catabolic, gluconeogenic, and lipogenic enzymes were measured in the liver of adult cats fed: a commercial kibble; a 17.5 or 70% protein purified diet, or starved for 5 days. Except for an increase in tyrosine transaminase (EC 2.6.1.5) after feeding the high protein diet, there were no changes in the activities of the hepatic enzymes as influenced by dietary protein level. Likewise, starvation had a minimal effect on the activities of these enzymes as compared to that found in similar experiments in rats. These results indicate that the cat may have only minimal capabilities for enzyme adaptation as compared to that found in many herbivores and omnivores and may provide an explanation as to why cats have an unusually high protein requirement as compared to many other mammals.

L3 ANSWER 7 OF 18 MEDLINE
ACCESSION NUMBER: 70151075 MEDLINE
DOCUMENT NUMBER: 70151075 PubMed ID: 5436140
TITLE: Molecular weight and amino acid composition of five-times-crystallized **phosphoglucose isomerase** from rabbit skeletal muscle.
AUTHOR: Pon N G; Schnackerz K D; Blackburn M N; Chatterjee G C; Noltmann E A
SOURCE: BIOCHEMISTRY, (1970 Mar 31) 9 (7) 1506-14.
Journal code: A0G; 0370623. ISSN: 0006-2960.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197005
ENTRY DATE: Entered STN: 19900101
Last Updated on STN: 19980206
Entered Medline: 19700510

L3 ANSWER 8 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:184754 CAPLUS
DOCUMENT NUMBER: 128:292608
TITLE: Determination of the carbon flux in the central metabolism of Corynebacterium glutamicum by 13C-isotope analysis
AUTHOR(S): Marx, Achim
CORPORATE SOURCE: Inst. Biotechnologie, Forschungszentrum Juelich G.m.b.H., Juelich, D-52425, Germany
SOURCE: Ber. Forschungszent. Juelich (1997), Juel-3459, 1-111 pp.
CODEN: FJBEE5; ISSN: 0366-0885
DOCUMENT TYPE: Report
LANGUAGE: German
AB All C fluxes of the central metab. of C. glutamicum were quantified and the role and coordination of single metabolic pathways were studied under different metabolic situations. A method based on 13C-data was established to quantify all metabolite fluxes of the central metab. Strong sensitivities were indicated between metabolic fluxes and 13C data, thus allowing the detn. of metabolite flux. When the 13C-content of the position oxalacetate C-4 was varied by the factor 2 it could be shown if anaplerotic prodn. of C4-bodies was via the carboxylation of C3-bodies or via the glyoxalate cycle. A hyperbolic relationship was shown for the bi-directional turnover of transketolase and the 13C-content of the position pentose-5-phosphate C-1 and for the bi-directional metabolite flux between C3-bodies of glycolysis and C4-bodies of the tricarboxylate (TCA) cycle and 13C-enrichment of the position oxalacetate C-2. The NADPH balance showed that, depending on the conditions, more NADPH was produced than necessary for the synthesis of biomass and products. The NADPH excess was 16-67% in relation to the glucose uptake rate. Depending on the metabolic situation, the C4-body-decarboxylation was 10-132% and opposed to the carboxylation of C3-bodies for the anaplerotic supply of the TCA cycle. C4-body-decarboxylation and NADPH-excess as adaptations to high prodn. of Lys were minimal, with a yield coeff. of 0.32 molLysmolglucose-1. The contribution of malate enzyme to a total NADPH prodn. of 211% was small. The pentose phosphate pathway (PPP) and the TCA cycle produced 3/4 and 1/4, resp., of the total NADPH. Overexpression of glutamate dehydrogenase in a mutant of strain MH20-22B resulted in low TCA cycle flux and a high metabolite flux through the oxidative PPP. A high TCA cycle flux was detected during glutamate prodn. using strain LE4. The PPP flux was low in this strain. In a mutant of strain MH20-22B producing Lys and using NADH for synthesis of glutamate, TCA cycle flux was 79% and that of PPP was 26%. The low PPP was due to low NADPH consumption and high NADPH prodn. from isocitrate dehydrogenase of the TCA cycle. A strain ATCC 13032 isocitrate dehydrogenase mutant with a blocked TCA cycle showed a PPP flux of 62%. This mutant showed a glyoxalate cycle active in vivo when metabolizing glucose. This metabolite flux was 53%. A flux of 16% produced anaplerotically C4-bodies. At a flux of 37% the glyoxalate cycle released CO2 by C4-body decarboxylation and pyruvate dehydrogenase.

L3 ANSWER 9 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:631539 CAPLUS
DOCUMENT NUMBER: 127:305184
TITLE: Physiological and NMR-spectroscopic investigations of in vivo activity of central metabolism pathways in wild and recombinant strains of Corynebacterium glutamicum
AUTHOR(S): Wendisch, Volker
CORPORATE SOURCE: Inst. Biotechnologie, Forschungszentrum Julich G.m.b.H., Juelich, D-52425, Germany
SOURCE: Ber. Forschungszent. Juelich (1997), Juel-3397, 1-111 pp.
CODEN: FJBEE5; ISSN: 0366-0885
DOCUMENT TYPE: Report
LANGUAGE: German
AB The C flux in the central metab. of C. glutamicum grown on glucose and/or acetate was detd. quant. and qual. The physiol. characterization of the growth of C. glutamicum revealed that this organism is able to metabolize acetate and glucose simultaneously. The C-uptake rates were quite similar with 900-1100 nmol C/mg protein. To analyze the C flux by 13C-labeling

expts., a new NMR-spectroscopic method was developed, calibrated, and applied. This 1H-spin-echo-NMR method for the detn. of 13C-labeled non-protonated C-atoms, for example in carboxyl groups of amino acids, is 4-8-fold more precise than conventional NMR methods. Qual. C flux analyses revealed that beside the PEP-carboxylase C. glutamicum possesses another anaplerotic C3-carboxylating reaction, a pyruvate carboxylase. In addn., an alternative acetate activation to the acetate-kinase-phosphotransacetylase way was found in C. glutamicum which is suggested an acetyl-CoA-synthetase. The C fluxes in the central metab. of C. glutamicum growing on glucose and/or acetate were quantified for the 1st time by 13C-labeling expts. and subsequent NMR-spectroscopic anal. of cellular amino acids in combination with the metabolite balance. The in vivo activities of the citrate synthase increased from 120 mU/mg protein on glucose to over 220 mU/mg protein on glucose plus acetate up to 410 mU/protein on acetate. The anaplerotic function was adopted by the PEP carboxylase and the pyruvate carboxylase at growth on glucose. At growth on acetate and surprisingly also at growth on glucose plus acetate, the glyoxylate cycle was active in vivo as the only anaplerotic sequence with 99 and 50 mU/mg protein, resp. The characterization of glyoxylate cycle-deficient C. glutamicum strains, which were produced by directed deletion of the genes for isocitrate lyase and the malate synthase, revealed that the glyoxylate cycle is essential for the optimal growth on glucose plus acetate. The glyoxylate cycle enzymes isocitrate lyase and malate synthase are regulated genetically by control of transcription of their genes aceA and aceB. High intracellular concns. of the metabolite acetyl-CoA correlated with high specific activities of the enzymes of the acetate metab.

L3 ANSWER 10 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:729783 CAPLUS
DOCUMENT NUMBER: 126:85324
TITLE: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
AUTHOR(S): Himmelreich, Ralf; Hilbert, Helmut; Plagens, Helga; Pirkl, Elsbeth; Li, Bi-Chen; Herrmann, Richard
CORPORATE SOURCE: Zenatrum Mol. Biologie Heidelberg, Univ. Heidelberg, Heidelberg, 69120, Germany
SOURCE: Nucleic Acids Res. (1996), 24(22), 4420-4449
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The entire genome of the bacterium Mycoplasma pneumoniae M129 has been sequenced. It has a size of 816 394 base pairs with an av. G+C content of 40.0 mol%. We predict 677 open reading frames (ORFs) and 39 genes coding for various RNA species. Of the predicted ORFs, 75.9% showed significant similarity to genes/proteins of other organisms while only 9.9% did not reveal any significant similarity to gene sequences in databases. This permitted us tentatively to assign a functional classification to a large no. of ORFs and to deduce the biochem. and physiol. properties of this bacterium. The redn. of the genome size of M. pneumoniae during its reductive evolution from ancestral bacteria can be explained by the loss of complete anabolic (e.g. no amino acid synthesis) and metabolic pathways. Therefore, M. pneumoniae depends in nature on an obligate parasitic lifestyle which requires the provision of exogenous essential metabolites. All the major classes of cellular processes and metabolic pathways are briefly described. For a no. of activities/functions present in M. pneumoniae according to exptl. evidence, the corresponding genes could not be identified by similarity search. For instance we failed to identify genes/proteins involved in motility, chemotaxis and management of oxidative stress.

L3 ANSWER 11 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1994:696921 CAPLUS
DOCUMENT NUMBER: 121:296921
TITLE: Multilocus isoenzyme diversity among strains of Pseudomonas cepacia isolated from decayed onions, soils, and clinical sources
AUTHOR(S): Yohalem, David S.; Lorbeer, James W.
CORPORATE SOURCE: New York State College Agriculture and Life Sciences, Cornell University, Ithaca, NY, 14853, USA
SOURCE: Syst. Appl. Microbiol. (1994), 17(1), 116-24
CODEN: SAMIDF; ISSN: 0723-2020
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A collection of 59 strains of Pseudomonas cepacia, isolated from a variety of clin. sources, from decayed onions, and from soils were characterized by multilocus isoenzyme electrophoresis and by pathogenic ability on onion. Fifty-three of the strains were found to be electrophoretically

unique accessions (DT = 0.981). An overall est. of genetic diversity, HT, of 0.620 was calcd., which is consistent with other published reports of diversity for the species. Less than two percent of the obsd. genetic diversity could be attributed to differences between clin. and environmental subpopulations, less than one percent to differences between phytopathogenic and nonphytopathogenic strains. Phytopathogens were absent from the clin. subpopulation. The extreme levels of obsd. within-group diversity combined with the behavioral differences between clin. and phytopathogenic strains suggest that isoenzymes are sufficient to function as strain identifiers, and that the present species concept of P. cepacia is too broad.

L3 ANSWER 12 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1994:101051 CAPLUS
DOCUMENT NUMBER: 120:101051
TITLE: Electrophoretic transfer from polyacrylamide gel to nitrocellulose sheets, a new method to characterize multilocus enzyme genotypes of Klebsiella strains
AUTHOR(S): Combe, Marie Laure; Pons, Jean Louis; Sesboue, Richard; Martin, Jean Pierre
CORPORATE SOURCE: Lab. Microbiol. Pharm., Univ. Rouen, Saint-Etienne Rouvray, F-76803, Fr.
SOURCE: Appl. Environ. Microbiol. (1994), 60(1), 26-30
CODEN: AEMIDF; ISSN: 0099-2240
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A new method for multilocus enzyme electrophoresis, based on electrophoretic transfers to nitrocellulose after polyacrylamide-agarose gel electrophoresis was explored. Electrophoretic sepn. was performed on 1-mm-thick slab gels with 6-.mu.L samples of bacterial exts. and was followed by serial 5-min consecutive transfers. The transferability of 19 metabolic enzymes of Klebsiella strains was studied and allowed the simultaneous examn. of one enzyme in the sepn. gel and at least five enzymes on nitrocellulose sheets. The resoln. of enzyme bands was increased on nitrocellulose; thus, well-sepd. bands were recorded for nucleoside phosphorylase, peptidase, and **phosphoglucose isomerase** whereas their mobility variants could not be clearly distinguished in the sepn. gel because of stain diffusion. The study of genetic relationships of 42 strains of Klebsiella pneumoniae and 24 strains of Klebsiella oxytoca demonstrated the reliability of the method, since clustering anal. of electrophoretic types, based on electrophoretic polymorphism of 10 metabolic enzymes, showed two main clusters well correlated with the two species. The 57 electrophoretic types described confirm the usefulness of the method for the study of genetic relationships between closely related strains.

L3 ANSWER 13 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1994:4325 CAPLUS
DOCUMENT NUMBER: 120:4325
TITLE: Salmonella reference collection B (SARB): Strains of 37 serovars of subspecies I
AUTHOR(S): Boyd, E. Fidelma; Wang, Fu Sheng; Beltran, Pilar; Plock, Sheila A.; Nelson, Kimberlyn; Selander, Robert K.
CORPORATE SOURCE: Inst. Mol. Evolut. Genet., Pennsylvania State Univ., University Park, PA, 16802, USA
SOURCE: J. Gen. Microbiol. (1993), 139(6), 1125-32
CODEN: JGMIAN; ISSN: 0022-1287
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A ref. collection of 72 strains representing 37 serovars of Salmonella subspecies I has been established for use in research on genetic and phenotypic variation in natural populations. Included are isolates of the host-adapted serovars S. choleraesuis, S. dublin, S. gallinarum, S. paratyphi A, S. paratyphi B, S. paratyphi C, S. pullorum, S. sendai, S. typhi and S. typhisuis, as well as strains of S. enteritidis, S. typhimurium, and other commonly recovered serovars with broad host ranges. The isolates were characterized by enzyme electrophoresis for allelic variation in 25 chromosomal genes and represent 71 distinctive multilocus genotypes (electrophoretic types or ETs). Genetic relationships among the ETs are indicated in an evolutionary tree constructed by the neighbor-joining method from a matrix of Nei's std. genetic distance.

L3 ANSWER 14 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1991:201961 CAPLUS
DOCUMENT NUMBER: 114:201961
TITLE: Purification and characterization of novel heparan sulfate proteoglycans produced by murine erythroleukemia cells in the growing phase

AUTHOR(S): Okayama, Minoru; Oguri, Kayoko; Yoshida, Keiichi; Ohkita, Takeshi
CORPORATE SOURCE: Clin. Res. Inst., Natl. Nagoya Hosp., Nagoya, 460, Japan
SOURCE: J. Biol. Chem. (1991), 266(6), 3808-19
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Murine erythroleukemia cells (Friend erythroleukemia cells of a C-10-6 line) synthesized sulfated glycosaminoglycans consisting mainly of heparan sulfate (more than 95%) with a small amt. of chondroitin 4-sulfate. The heparan sulfate occurred as proteoglycans, of which the cell-assocd. component was sepd. into urea-insol. (UI) and urea-sol. (US) fractions. The UI proteoglycan consisted of a single homogeneous mol. species with an estd. Mr of 360,000 (C(UI)PG), whereas the US component was composed of two subfractions: a homogeneous species with an Mr of 280,000 (C(US) **PGI**) and a mixt. of compds. with Mr values of less than 80,000 (C(US)PGII), which were isolated in yields of about 110, 340, and 80 .mu.g of hexuronate (HexUA), resp., from 1.37 g of an acetone powder prepd. from 5.7 .times. 109 cells in the logarithmic phase of growth. The proteoglycan released into the medium (12 L) was a single homogeneous species with an Mr of 320,000 (MPG) which was purified in a yield of 500 .mu.g of hexuronate. The major, cell-assocd. proteoglycan, C(US) **PGI**, had very high contents of serine and glycine, accounting for approx. 80% of the total amino acids. This proteoglycan as well as the other two large proteoglycans, C(UI)PG and MPG, were highly resistant to degrdn. by various proteinases. These three proteoglycans, C(UI)PG, C(US) **PGI**, and MPG, and heparan sulfates with estd. Mr values of 32,000, 27,000, and 30,000. On the other hand, the Mr of the smaller proteoglycan, C(UI)PGII, was not significantly different before and after .beta.-elimination, indicating that it contains only a small peptide, if any. The heparan sulfate of this proteoglycan consisted of smaller and heterogeneous mol. species with Mr values of 26,000, 20,000, and 4,000. Digestion of these heparan sulfates with heparitinase I plus II resulted in almost complete depolymn. and gave six unsatd. disaccharides, .DELTA.HexUA-GlcNAc, .DELTA.HexUA-GlcNAc(6-SO4), .DELTA.HexUA-GlcNSO3, .DELTA.HexUA-GlcNSO3(6-SO4), .DELTA.HexUA(2-SO4)-GlcNSO3, and .DELTA.HexUA(2-SO4)-GlcNSO3(6-SO4). The relative amts. of these disaccharides generated from the individual heparan sulfates showed that an av. ratio of sulfate residues to repeating disaccharide units of the C(US)PGII-derived heparan sulfate (0.97) was significantly higher than those of the other three large proteoglycan-derived glycosaminoglycans (0.54-0.70).

L3 ANSWER 15 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1991:160534 CAPLUS
DOCUMENT NUMBER: 114:160534
TITLE: Genetic relationships among strains of avian Escherichia coli associated with swollen-head syndrome
AUTHOR(S): White, David G.; Wilson, Richard A.; San Gabriel, Alberto; Saco, Montserrat; Whittam, Thomas S.
CORPORATE SOURCE: Inst. Mol. Evol. Genet., Pennsylvania State Univ., University Park, PA, 16802, USA
SOURCE: Infect. Immun. (1990), 58(11), 3613-20
CODEN: INFIBR; ISSN: 0019-9567
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Genetic diversity among 22 E. coli strains isolated from chickens with swollen-head syndrome (SHS), an acute respiratory disease of domestic poultry, and 93 strains isolated from birds with colibacillosis was assessed on the basis of allelic variation at 20 enzyme-encoding loci detected by multilocus enzyme electrophoresis. SHS isolates from Spain and Canada were polymorphic at 14 loci and were classified into 19 multilocus genotypes, defining clones that differed on av. at 34% of the loci. In most cases, SHS isolates of different clonal genotypes were distinct in O:H serotype and expressed different fimbrial antigens. Comparisons with 93 isolates obtained from birds with colibacillosis revealed enzyme polymorphisms at 17 of 20 loci, with an av. of 3.5 alleles per locus. In the total sample, 56 clonal genotypes were distinguished, with 27 (23%) of the isolates belonging to one of three common clones. Both SHS and colibacillosis isolates were genetically diverse, with an av. single-locus diversity of 0.36, indicating that a wide variety of naturally occurring bacterial clones is assocd. with these acute avian infections. Six previously defined groups of clones identified in diseased birds from the United States were represented in isolates from Spain, indicating that similar clones occur in widely sepd. geog. areas. In addn., one group of SHS isolates was closely related to a recognized widespread clone complex incriminated in human septicemia and meningitis. The results suggest that certain strains implicated in SHS infections

belong to a clone complex whose members have special attributes that promote involvement in invasive diseases in humans and animals.

L3 ANSWER 16 OF 18 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1993:460868 BIOSIS
DOCUMENT NUMBER: PREV199396105768
TITLE: Comparison of the effects of prostanoids on human penile circumflex veins and corpus cavernosum tissue.
AUTHOR(S): Kirkeby, H. J. (1); Anderson, K.-E.; Forman, A.
CORPORATE SOURCE: (1) Gynaecological Res. Lab., Aarhus Kommunehospital, DK-8000 Aarhus C Denmark
SOURCE: British Journal of Urology, (1993) Vol. 72, No. 2, pp. 220-225.
ISSN: 0007-1331.
DOCUMENT TYPE: Article
LANGUAGE: English
AB The mechanical effects of the prostaglandins PGE-1, PGE-2, PGF-2alpha and **PGI**-2 were investigated in human isolated penile circumflex veins (CV) and corpus cavernosum (CC) tissue. PGE-1 did not affect resting tension, while the compound produced relaxation of both CC and CV preparations after precontraction with noradrenaline (NA) 3 times 10-6 M. PGE-2 produced contraction in CC and CV preparations. After precontraction with NA, however, relaxation was induced in both tissues. PGF-2alpha induced contraction in CC and CV preparations, while no relaxant responses were seen in preparations precontracted with NA. **PGI**-2 produced no mechanical effects in unstimulated CV preparations, whereas dose-related contraction was induced in CC tissue strips. After precontraction with NA, **PGI**-2 showed no effect in 2 of 6 CC preparations, while relaxation was seen in 4. In CV preparations precontracted with NA, **PGI**-2 produced relaxation. Local synthesis of prostanoids may influence resting tension and modulate NA-induced responses not only in human penile CC but also in CV smooth muscle.

L3 ANSWER 17 OF 18 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1991:348257 BIOSIS
DOCUMENT NUMBER: BA92:47632
TITLE: EFFECTS OF OKADAIC ACID ON AGONIST-STIMULATED **PGI** -2 PRODUCTION BY RAT LIVER CELLS THE C-9 CELL LINE.
AUTHOR(S): LEVINE L
CORPORATE SOURCE: DEP. BIOCHEMISTRY, BRANDEIS UNIV., WALTHAM, MASS. 02254.
SOURCE: PROSTAGLANDINS, (1991) 41 (6), 615-624.
CODEN: PRGLBA. ISSN: 0090-6980.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Preincubation of rat liver cells (the C-9 cell line) with okadaic acid (0.6 .mu.M), a known inhibitor of protein-serine/**threonine** phosphate phosphatases 2A and 1, for 30 min amplified 6-keto-PGF1.alpha. production stimulated by thapsigargin, thrombin, platelet activating factor (PAF), 12-O-tetradecanoylphorbol-13-acetate (TPA), the Ca2+ ionophore A-23187 and lysine-vasopressin (Lys .cntdot. ADH) but not the stimulated by exogenous arachidonic acid. The amplification occurred within minutes after addition of the stimulators. The effect of preincubation was time dependent. Preincubation of the cells with okadiac acid (0.6 .mu.M) for longer than 30 min decreased this amplication. The results suggest that inhibition of protein-serine/**threonine** phosphates phosphatase(s) can both positively and negatively regulate dessterification of phospholipids although the negative regulation may reflectr a toxic response. Microcystin LR and nodularin, inhibitors of protein-serine/**threonine** phosphate phosphatases 2A and 1 in vitro, did not amplify 6-keto-PGF1.alpha. production by PAF when incubated with intact cells.

L3 ANSWER 18 OF 18 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1977:224544 BIOSIS
DOCUMENT NUMBER: BA64:46908
TITLE: PATHWAYS OF NADPH FORMATION OF ESCHERICHIA-COLI.
AUTHOR(S): CSONKA L N; FRAENKEL D G
SOURCE: J BIOL CHEM, (1977) 252 (10), 3382-3391.
CODEN: JBCHA3. ISSN: 0021-9258.
FILE SEGMENT: BA; OLD
LANGUAGE: Unavailable
AB NADPH formation during growth on glucose was studied in wild type E. coli and in mutants affected, directly or indirectly, in the NADPH-forming reactions glucose-6-phosphate dehydrogenase, isocitrate dehydrogenase, malate dehydrogenase and energy-linked transhydrogenase. The main technique was to grow cells in media containing glucose labeled uniformly with 14C and also containing glucose tritiated specifically at positions 1, 3, 4 or 6. Amino acids were isolated from protein and their 3H/14C

ratios determined. For **threonine** and aspartate, or proline and glutamate, which differ by 2 NADPH-dependent reductions, the contribution of H from each glucose position to the reductions could be calculated from the difference in 3H/14C ratios. In some experiments 3H/14C ratios were determined for the fatty acid fraction, and in anaerobic experiments ethanol was isolated. A strain lacking both glucose-6-phosphate dehydrogenase and isocitrate dehydrogenase still grew on glucose aerobically and anaerobically. Even in a glucose-6-phosphate dehydrogenase mutant or anaerobically in an isocitrate dehydrogenase mutant, H from the 1 and 6 positions of glucose contributed to the biosynthetic reducing pool NADPH. In the wild type strain, the 3 position H of glucose also appeared in NADPH; that contribution was lower in anaerobiosis and was absent in a glucose-6-phosphate dehydrogenase mutant. In a **phosphoglucose isomerase** mutant, H from the 1 and 3 positions of glucose made greater contribution to NADPH than in the wild type strain; a mutant lacking both **phosphoglucose isomerase** and the membrane ATPase did not grow on glucose. H from the 4 position of glucose was a major contributor to NADH, as shown by radioactivity in ethanol. That H was a minor source of NADPH; the contribution to NADPH was absent in an ATPase mutant uncB. Accordingly, the hexose monophosphate shunt is probably a minor pathway of NADPH formation in wild type E. coli. The main source of the hydride of NADPH is H from the 1 and 6 positions of glucose, by a pathway not identified. NADH is a minor source of NADPH, possibly via the energy-linked transhydrogenase. In a **phosphoglucose isomerase** mutant, the hexose monophosphate shunt is a major source of NADPH, in which case the energy-linked transhydrogenase might be used in NADPH oxidation.

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